

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: BAYLOR COLLEGE OF MEDICINE  
SMITH, JAMES R.

(ii) TITLE OF INVENTION: SENESCENT CELL DERIVED  
INHIBITORS OF DNA SYNTHESIS

10

(iii) NUMBER OF SEQUENCES: 36

(iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: HOWREY & SIMON  
(B) STREET: 1299 PENNSYLVANIA AVENUE, N.W.  
(C) CITY: WASHINGTON  
(D) STATE: D.C.  
(E) COUNTRY: USA  
(F) ZIP: 20004

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE:  
30 (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/808,523  
(B) FILING DATE: 16-DEC-1991

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 07/970,462  
(B) FILING DATE: 02-NOV-1992

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/113,372  
(B) FILING DATE: 30-AUG-1993

1000000-00000001

(B) FILING DATE: 17-NOV-1993

(B) FILING DATE: 25-FEB-1994

(B) FILING DATE: 15-APR-1994

15 (B) FILING DATE: 13-JUL-1994

(B) FILING DATE: 26-AUG-1994

(C) REFERENCE/DOCKET NUMBER: 225-102-CIP9

(B) TELEFAX: (202) 383-6610

(D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO



25 (2) INFORMATION FOR SEQ ID NO:2:

## 30

(D) TOPOLOGY: linear

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(iv) ANTI-SENSE: NO

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(B) STRAIN: SDI-1

(A) LIBRARY: Senescent cell derived cDNA library

Met Ser Glu Pro Ala Gly Asp Val Arg Gln Asn Pro Cys Gly Ser Lys  
1 5 10 15

50 Ala Cys Arg Arg Leu Phe Gly Pro Val Asp Ser Glu Gln Leu Ser Arg  
20 25 30

Asp Cys Asp Ala Leu Met Ala Gly Cys Ile Gln Glu Ala Arg Glu Arg  
 35 40 45  
 5 Trp Asn Phe Asp Phe Val Thr Glu Thr Pro Leu Glu Gly Asp Phe Ala  
 50 55 60  
 Trp Glu Arg Val Arg Gly Leu Gly Leu Pro Lys Leu Tyr Leu Pro Thr  
 65 70 75 80  
 10 Gly Pro Arg Arg Gly Arg Asp Glu Leu Gly Gly Gly Arg Arg Pro Gly  
 85 90 95  
 Thr Ser Pro Ala Leu Leu Gln Gly Thr Ala Glu Glu Asp His Val Asp  
 100 105 110  
 15 Leu Ser Leu Ser Cys Thr Leu Val Pro Arg Ser Gly Glu Gln Ala Glu  
 115 120 125  
 Gly Ser Pro Gly Gly Pro Gly Asp Ser Gln Gly Arg Lys Arg Arg Gln  
 130 135 140  
 20 Thr Ser Met Thr Asp Phe Tyr His Ser Lys Arg Arg Leu Ile Phe Ser  
 145 150 155 160  
 25 Lys Arg Lys Pro

(2) INFORMATION FOR SEQ ID NO:3:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: HOMO SAPIENS

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGCCGGTTCT GACATGCCG

19

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(2) INFORMATION FOR SEQ ID NO:4:

1000960.120701

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(v) FRAGMENT TYPE: N-terminal

(vii) IMMEDIATE SOURCE:

(B) CLONE: [His]6 leader peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Gly	Ser	His	His	His	His	His	His	Gly	Ala
1				5					10		

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 699 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Schistosoma japonicum

(vii) IMMEDIATE SOURCE:

(B) CLONE: GST

1000960-120701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5 ATGTCCCCTA TACTAGGTTA TTGGAATAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60  
 TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTGTATG AGCGCGATGA AGGTGATAAA 120  
 TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT 180  
 10 GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAAC 240  
 ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTTCOA TGCTTGAAGG AGCGGTTTTG 300  
 15 GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360  
 GATTTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTTCG AAGATCGTTT ATGTCATAAA 420  
 ACATATTTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTTGTATGA CGCTCTTGAT 480  
 20 GTTGTTTTAT ACATGGACCC AATGTGCCTG GATGCGTTC CAAAATTAGT TTGTTTTAAA 540  
 AAACGTATTG AAGCTATCCC ACAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA 600  
 25 TGGCCTTTGC AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT 660  
 CTGGTTCCGC GTGGATCCCC GGGAATTCAT CGTGACTGA 699

(2) INFORMATION FOR SEQ ID NO:6:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 232 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: NO
- (vi) ORIGINAL SOURCE:  
 40 (A) ORGANISM: Schistosoma japonicum
- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: GST

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15

50 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30

100090.1200

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## 45

- (A) LENGTH: 13 base pairs**

- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear

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- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO



(vii) IMMEDIATE SOURCE:

(B) CLONE: linker fragment for GST-SDI-1 gene fusion

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGATCCCCC GCC

13

(2) INFORMATION FOR SEQ ID NO:8:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

20

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: linker fragment for GST-SDI-1 gene fusion

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCTCGAGGG

10

30 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids

(B) TYPE: amino acid

35

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

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(v) FRAGMENT TYPE: internal

10009901-0968001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Arg Gly Asp Pro Pro Ala  
1 5

10

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GTCCGTCAGA ACCCATGCGG CAGCAAGGCC TGCCGCCGCC TCTTCGGCCC AGTGGACAGC 780

5 GAGCAGCTGA GCCGCGACTG TGATGCGCTA ATGGCGGGCT GCATCCAGGA GGCCCGTGAG 840  
 CGATGGAACT TCGACTTTGT CACCGAGACA CCACTGGAGG GTGACTTCGC CTGGGAGCGT 900  
 GTGCGGGGCC TTGGCCTGCC CAAGCTCTAC CTTCCACGG GGGCCCGGCG AGGCCGGGAT 960  
 GAGTTGGGAG GAGGCAGGCG GCCTGGCACC TCACCTGCTC TGCTGCAGGG GACAGCAGAG 1020  
 10 GAAGACCATG TGGACCTGTC ACTGTCTTGT ACCCTTGTGC CTCGCTCAGG GGAGCAGGCT 1080  
 GAAGGGTCCC CAGGTGGACC TGGAGACTCT CAGGGTCGAA AACGGCGGCA GACCAGCATG 1140  
 ACAGATTCTT ACCACTCCAA ACGCCGGCTG ATCTTCTCCA AGAGGAAGCC CTAA 1194  
 15

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 397 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25 (iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: GST-SDI-1 fusion protein

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15  
 35 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 40 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 45 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 50 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125

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	Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn
	130						135					140				
5	Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp
	145					150					155					160
	Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu
					165					170					175	
10	Val	Cys	Phe	Lys	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr
				180					185					190		
	Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala
15			195					200					205			
	Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg
	210						215					220				
20	Gly	Ser	Pro	Arg	Gly	Asp	Pro	Pro	Ala	Met	Ser	Glu	Pro	Ala	Gly	Asp
	225					230					235					240
	Val	Arg	Gln	Asn	Pro	Cys	Gly	Ser	Lys	Ala	Cys	Arg	Arg	Leu	Phe	Gly
					245					250					255	
25	Pro	Val	Asp	Ser	Glu	Gln	Leu	Ser	Arg	Asp	Cys	Asp	Ala	Leu	Met	Ala
				260					265					270		
	Gly	Cys	Ile	Gln	Glu	Ala	Arg	Glu	Arg	Trp	Asn	Phe	Asp	Phe	Val	Thr
30			275					280					285			
	Glu	Thr	Pro	Leu	Glu	Gly	Asp	Phe	Ala	Trp	Glu	Arg	Val	Arg	Gly	Leu
	290						295				300					
35	Gly	Leu	Pro	Lys	Leu	Tyr	Leu	Pro	Thr	Gly	Pro	Arg	Arg	Gly	Arg	Asp
	305					310					315					320
	Glu	Leu	Gly	Gly	Gly	Arg	Arg	Pro	Gly	Thr	Ser	Pro	Ala	Leu	Leu	Gln
					325					330					335	
40	Gly	Thr	Ala	Glu	Glu	Asp	His	Val	Asp	Leu	Ser	Leu	Ser	Cys	Thr	Leu
			340						345					350		
	Val	Pro	Arg	Ser	Gly	Glu	Gln	Ala	Glu	Gly	Ser	Pro	Gly	Gly	Pro	Gly
45			355					360					365			
	Asp	Ser	Gln	Gly	Arg	Lys	Arg	Arg	Gln	Thr	Ser	Met	Thr	Asp	Phe	Tyr
	370						375					380				
50	His	Ser	Lys	Arg	Arg	Leu	Ile	Phe	Ser	Lys	Arg	Lys	Pro			
	385					390					395					

(2) INFORMATION FOR SEQ ID NO:12:

55 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs





(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

15

TTCGGCCCTC GAGGCCTGAG CCGCGACTGT

30

(2) INFORMATION FOR SEQ ID NO:17:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTCAGGCCT CGAGGGCCGA AGAAGCGGCG

30

(2) INFORMATION FOR SEQ ID NO:18:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

15

TTAGCGCGCC TCGAGGCTGC TCGCTGTCCA C

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

35

CGAGCAGCCT CGAGGCGCGC TAATGGCGGG C

31

(2) INFORMATION FOR SEQ ID NO:20:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

1000960.120701



(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10 (vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCTGCCCTC GAGGCCGATG GAACTTCGAC

30

15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

30 (vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35 CCATCGGCCT CGAGGGCAGC CCGCCATTAG

30

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTGAGCGAC CCCGGGGCGT CACCGAGACA CCACTG

36

15 (2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

30

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCGGTGACG CCCCGGGGTC GCTCAGGGC CTCCTG

36

35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

40

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

5 (iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTCGACCCCTC GAGGCCTGGA GGGTGACTTC

30

(2) INFORMATION FOR SEQ ID NO:25:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCCAGGCCT CGAGGGTCGA AGTTCCATCG

30

35 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

10

ACCGAGACAT CCCGGGCCGA CTCGCCTGG GAGCGT

36

(2) INFORMATION FOR SEQ ID NO:27:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

25

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GCCGAAGTCG GCCCGGGATG TCTCGGTGAC AAAGTC

36

(2) INFORMATION FOR SEQ ID NO:28:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

10 CCACTGGAGC CCCGGGGCCG TGTGCGGGC CTTGGC

36

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25 (vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

30 CCGCACACGG CCCCGGGGCT CCA GTGGTGT CTCGGT

36

(2) INFORMATION FOR SEQ ID NO:30:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

1000950-12001

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

5 (B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCTGGCCTC GAGGCGGCCT GCCCAAGCTC

30

10

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: cDNA

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

25

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAGGCCGCCT CGAGGCCAGG CGAAGTCACC

30

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: cDNA

40

(iii) HYPOTHETICAL: NO

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(vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

41

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20 (iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

40

(2) INFORMATION FOR SEQ ID NO:34:

35 (A) LENGTH: 29 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

40 (iii) HYPOTHETICAL: NO

(v) **FRAGMENT TYPE:** internal

(vii) IMMEDIATE SOURCE:

(B) CLONE: peptide mimetic fragment

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5

Trp Asn Phe Asp Phe Xaa Xaa Xaa Xaa Pro Leu Glu Gly Xaa Xaa Xaa  
1 5 10 15

10

Trp Xaa Xaa Val Xaa Xaa Xaa Xaa Leu Pro Xaa Xaa Tyr  
20 25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

30

CAGAATCACA AGCCACTCGA GGGTAAGTAC GAGTGGGAGC GTGTGCGGGG CCTT

54

(2) INFORMATION FOR SEQ ID NO:36:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

1000660.120701



(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: Primer

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTACCCTCG AGTGGCTTGT GATTCTGAAA GTCGAAGTTC CATCGCTC

48

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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